```
Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: [year=2009; month=11; day=4; hr=9; min=21; sec=49; ms=542; ]
______
****************
Reviewer Comments:
<160> 66
Although the above <160> response is "66", 68 sequences are in the
submitted file. Please see below:
<210> 68
<211> 10
<212> PRT
<213> Saccharomyces cerevisiae
<400> 68
Glu Arg Trp Ile Trp Ile Arg Ser Gly Thr
             5
                              1.0
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The above is the last sequence in the submitted file.

## Validated By CRFValidator v 1.0.3

Application No: 10575374 Version No: 2.0

Input Set:

Output Set:

Started: 2009-10-21 17:32:28.305 Finished: 2009-10-21 17:32:30.540

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 235 ms

Total Warnings: 48

Total Errors: 2

No. of SeqIDs Defined: 66

Actual SeqID Count: 68

Error code		Error Description										
Е	257	Invalid sequence data feature in <221> in SEQ ID (15)										
W	213	Artificial or Unknown found in <213> in SEQ ID (19)										
W	213	Artificial or Unknown found in <213> in SEQ ID (20)										
W	213	Artificial or Unknown found in <213> in SEQ ID (21)										
W	213	Artificial or Unknown found in <213> in SEQ ID (22)										
W	213	Artificial or Unknown found in <213> in SEQ ID (23)										
W	213	Artificial or Unknown found in <213> in SEQ ID (24)										
W	213	Artificial or Unknown found in <213> in SEQ ID (25)										
W	213	Artificial or Unknown found in <213> in SEQ ID (26)										
W	213	Artificial or Unknown found in <213> in SEQ ID (27)										
W	213	Artificial or Unknown found in <213> in SEQ ID (28)										
W	213	Artificial or Unknown found in <213> in SEQ ID (29)										
W	213	Artificial or Unknown found in <213> in SEQ ID (30)										
W	213	Artificial or Unknown found in <213> in SEQ ID (31)										
W	213	Artificial or Unknown found in <213> in SEQ ID (32)										
W	213	Artificial or Unknown found in <213> in SEQ ID (33)										
W	213	Artificial or Unknown found in <213> in SEQ ID (34)										
W	213	Artificial or Unknown found in <213> in SEQ ID (35)										
W	213	Artificial or Unknown found in <213> in SEQ ID (36)										
W	213	Artificial or Unknown found in <213> in SEQ ID (37)										

## Input Set:

#### Output Set:

**Started:** 2009-10-21 17:32:28.305 **Finished:** 2009-10-21 17:32:30.540

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 235 ms

Total Warnings: 48
Total Errors: 2

No. of SeqIDs Defined: 66

Actual SeqID Count: 68

Error code		Error Description									
W	213	Artificial or Unknown found in <213> in SEQ ID (38) This error has occured more than 20 times, will not be displayed									
E	252	Calc# of Seg. differs from actual: 66 segIds defined: count=68									

#### SEQUENCE LISTING

<110>	Ecole Polytech	nique Federa	ale de Laus	anne (EPFL)										
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	10575374 2009-10-21													
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	-													
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	site													
<300>														
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\303Z	2004-00-30													
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	-													
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aaagca	ata aaaatagtto	aggcactccg	aaatacttgg	ttggcgtgtt	tcgtaatcaa	240								
cctaag	gagg atgttttggc	tctggtcaat	gattacggca	ttgatatcgt	ccaactgcac	300								
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gtattt	ccaa aagactgcaa	catactactc	agtgcagctt	cacagaaacc	teattegttt	420								
attece	tgt ttgattcaga	agcaggt ggg	acaggtgaac	ttttggattg	gaactcgatt	480								
tctgac	ggg ttggaaggca	agagageeee	gagagettae	attttatgtt	agctggtgga	540								
ctgacg	ccag aaaatgttgg	tgatgcgctt	agattaaatg	gcgttattgg	tgttgatgta	600								
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<309> 2004-08-30
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       20 25 30
Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
    35 40 45
Asp Pro Val Ile Ala Arc Lvs Ile Ser Ser Leu Val Lvs Ala Tvr Lvs
            55
Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln
65 70 75 80
Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile
         85
                90 95
Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu
       100 105 110
Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile
    115 120 125
Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe
 130 135 140
Asp Ser Glu Ala Glv Glv Thr Glv Glu Leu Leu Asp Trp Asn Ser Ile
       150
                    155
Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met
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170

175

165

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Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu
                           185
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                   215
                                      220
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<223> point mutation
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agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt
                                                              120
gtgcccaata ga
                                                               132
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          5
                             10
                                                 15
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          20 25 30
Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg
      35
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qttttqqctc tqqtcaatqa ttacqqcatt qatatcqtcc aactqcacqq aqatqaqtcq
tggcaagaat accaagagtt cctcggtttg ccagttatta aaagactcgt atttccaaaa
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aatgttggtg atgcgcttag attaaatggc gttattggtg ttgatgtaag cggaggtgtg
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<213> Saccharomyces cerevisiae
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          5
Lys Ala Tyr Lys Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val
           20
Phe Arg Asn Gln Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr
       35
                        40
                                             45
Gly Ile Asp Ile Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr
Gln Glu Phe Leu Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys
                 7.0
App Cys Acn Ile Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe
              85
                               90
Ile Pro Leu Phe Asp Ser Glu Ala Glv Glv Thr Glv Glu Leu Leu Asp
                             105
           100
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Trp Asn Ser Ile Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser

125

120

115

60

120

180

240

300

360

480

```
Leu His Phe Met Leu Ala Glv Glv Leu Thr Pro Glu Asn Val Glv Asp
                  135
Ala Leu Arg Leu Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val
145
              150
                        155
                                           160
Glu Thr Asn Gly Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val Lys
            165
                     170 175
Asn Ala Lys Lys
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<213> Saccharomyces cerevisiae
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agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt
                                                           120
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                                                           159
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<213> Saccharomyces cerevisiae
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                         10
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        20
               25
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     35
             40
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  50
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<212> DNA

# <213> Saccharomyces cerevisiae

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516

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<212> PRT

<213> Saccharomyces cerevisiae

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Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys Asn Ser Ser Gly 1  $$10\,$ 

Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln Pro Lys Glu Asp \$20\$

Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile Val Gln Leu His 35 40 45

Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu Gly Leu Pro Val 50 55 60

Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile Leu Leu Ser Ala 65 70 75 80

Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe Asp Ser Glu Ala 85 90 95

Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile Ser Asp Trp Val  $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110$ 

Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met Leu Ala Gly Gly 115 120 125	
Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu Asn Gly Val Ile 130 135 140	
Gly Val Asp Val Ser Gly Gly Val Glu Thr Asm Gly Val Lys Asp Ser 145 150 155 160	
Asm Lys Ile Ala Asm Phe Val Lys Asm Ala Lys Lys 165 170	
<210> 11 <211> 561 <212> DNA <213> Gaccharomyces cerevisiae	
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gtgcccaata gaaagagaac aattgacccg gttattgcaa ggaaaatttc aagtcttgta	180
aaagettata aaaatagtte aggeacteeg aaataettgg ttggegtgtt tegtaateaa	240
cctaaggagg atgttttggc tctggtcaat gattacggca ttgatatcgt ccaactgcac	300
ggagatgagt cgtggcaaga ataccaagag ttcctcggtt tgccagttat taaaagactc	360
gtatttccaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcgttt	420
attcccttgt ttgattcaga agcaggtggg acaggtgaac ttttggattg gaactcgatt	480
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Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser A: 20 25 30

Ala	Asp	Leu 35	Leu	Gly	Ile		Cys 40	Val	Pro	Asn	Arg	Lys 45	Arg	Thr	Ile		
	Pro 50	Val	Ile	Ala	Arg	Lys 55	Ile	Ser	Ser		Val 60	Lys	Ala	туг	Lys		
Asn 65	Ser	Ser	Gly	Thr	Pro 70	Lys	Tyr	Leu		Gly 75	Val	Phe	Arg	Asn	Gln 80		
Pro	Lys	Glu		Val 85	Leu	Ala	Leu		Asn 90	Asp	туг	Gly	Ile	Asp 95	Ile		
Val	Gln	Leu	His 100		Asp	Glu	Ser	Trp 105	Gln	Glu	Tyr	Gln	Glu 110	Phe	Leu		
Gly	Leu	Pro 115		Ile	Lys		Leu 120		Phe	Pro		Asp 125	Cys	Asn	Ile		
	Leu 130	Ser	Ala	Ala		Gln 135		Pro	His		Phe 140	Ile	Pro	Leu	Phe		
Asp 145	Ser	Glu	Ala	Gly	Gly 150		Gly	Glu		Leu 155		Trp	Asn	Ser	Ile 160		
Ser	Asp	Trp		Gly 165		Gln	Glu		Pro 170	Glu	Ser	Leu	His	Phe 175	Met		
Leu	Ala	Gly	Gly 180	Leu	Thr	Pro	Glu	Asn 185	Val	Gly							
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ggtg	gtaa	nag a	actet	aaca	ia aa	tago	caaat	: tto	egtea	ıaaa	atgo	ctaaq	gaa a	a		111	
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ctgacgccag aaaatgttgg tgatgcgctt agattaaatg gcgttattgg tgttgatgta

600

612

ageggaggtg tg

<211> 204

<213> Saccharomyces cerevisiae

<400> 16

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Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp  $20 \hspace{1.5cm} 25 \hspace{1.5cm} 30$ 

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys  $50 \ \ 55 \ \ 60$ 

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln 65 70 75 80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile 85 90 95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu \$100\$

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile 115 120 125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe 130 135 140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile 145 \$150\$

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met 165 170 175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu 180 185 190

Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val

195 200

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aacaaaatag caaatttcgt caaaaatgct aagaaa
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<211> 12
<212> PRT
<213> Saccharomyces cerevisiae
<400> 18
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1 5
<210> 19
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<213> Artificial Sequence
<220>
<223> first of a pair of peptides (together with peptide C2), that asso
      ciate into an anti-parallel coiled coil (Biochemistry 37 (1998),
      12603-12610)
<400> 19
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           5
                               10
                                                  15
Gln Asn Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Leu
         20 25 30
Glu Lys Glu Leu Gln Ala Gly Ser Gly Ser Gly
      35
<210> 20
<211> 50
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<213> Artificial Sequence
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Lys Leu Gln Ala Gly Ser Tyr Pro Tyr Asp